Anton Khmelinskii

List of Publications by Year
in descending order

30	2,037	331259	476904
papers	citations	21 h-index	29 g-index

36	36	36	3071
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Up-regulation of ubiquitinâ€“proteasome activity upon loss of NatA-dependent N-terminal acetylation. Life Science Alliance, 2022, 5, e202000730.	1.3	11
2	High-Throughput Analysis of Protein Turnover with Tandem Fluorescent Protein Timers. Methods in Molecular Biology, 2022, 2378, 85-100.	0.4	3
3	Quality control of mislocalized and orphan proteins. Experimental Cell Research, 2021, 403, 112617.	1.2	11
4	Timer-based proteomic profiling of the ubiquitin-proteasome system reveals a substrate receptor of the GID ubiquitin ligase. Molecular Cell, 2021, 81, 2460-2476.e11.	4.5	39
5	Exploring whole-genome duplicate gene retention with complex genetic interaction analysis. Science, 2020, 368, .	6.0	79
6	Ubc13-Mms2 cooperates with a family of RING E3s in membrane protein sorting. Journal of Cell Science, 2020, 133, .	1.2	11
7	(Photo)convert to pooled visual screening. Molecular Systems Biology, 2020, 16, e9640.	3.2	0
8	Cooperation of mitochondrial and ER factors in quality control of tail-anchored proteins. ELife, 2019, 8, .	2.8	68
9	Mapping Degradation Signals and Pathways in a Eukaryotic N-terminome. Molecular Cell, 2018, 70, 488-501.e5.	4.5	80
10	Determinants of the cytosolic turnover of mitochondrial intermembrane space proteins. BMC Biology, 2018, 16, 66.	1.7	45
11	Genome-wide C-SWAT library for high-throughput yeast genome tagging. Nature Methods, 2018, 15, 598-600.	9.0	57
12	Temporal and compartment-specific signals coordinate mitotic exit with spindle position. Nature Communications, 2017, 8, 14129.	5.8	15
13	Upregulation of SPS100 gene expression by an antisense RNA via a switch of mRNA isoforms with different stabilities. Nucleic Acids Research, 2017, 45, 11144-11158.	6.5	5
14	Protein Abundance Control by Non-coding Antisense Transcription. Cell Reports, 2016, 15, 2625-2636.	2.9	51
15	Incomplete proteasomal degradation of green fluorescent proteins in the context of tandem fluorescent protein timers. Molecular Biology of the Cell, 2016, 27, 360-370.	0.9	72
16	One library to make them all: streamlining the creation of yeast libraries via a SWAp-Tag strategy. Nature Methods, 2016, 13, 371-378.	9.0	171
17	Protein quality control at the inner nuclear membrane. Nature, 2014, 516, 410-413.	13.7	188
18	Analytical model for macromolecular partitioning during yeast cell division. BMC Biophysics, 2014, 7, 10.	4.4	10

#	Article	IF	Citations
19	A Memory System of Negative Polarity Cues Prevents Replicative Aging. Cell, 2014, 159, 1056-1069.	13.5	50
20	Analysis of Protein Dynamics with Tandem Fluorescent Protein Timers. Methods in Molecular Biology, 2014, 1174, 195-210.	0.4	36
21	Directional tissue migration through a self-generated chemokine gradient. Nature, 2013, 503, 285-289.	13.7	320
22	Tandem fluorescent protein timers for in vivo analysis of protein dynamics. Nature Biotechnology, 2012, 30, 708-714.	9.4	239
23	Artificial tethering to nuclear pores promotes partitioning of extrachromosomal DNA during yeast asymmetric cell division. Current Biology, 2011, 21, R17-R18.	1.8	38
24	Seamless Gene Tagging by Endonuclease-Driven Homologous Recombination. PLoS ONE, 2011, 6, e23794.	1.1	56
25	Segregation of yeast nuclear pores. Nature, 2010, 466, E1-E1.	13.7	45
26	Cell cycle control of spindle elongation. Cell Cycle, 2010, 9, 1084-1090.	1.3	32
27	Chromosome Segregation: Monopolin Goes Spindle. Current Biology, 2009, 19, R482-R484.	1.8	1
28	Phosphorylation-Dependent Protein Interactions at the Spindle Midzone Mediate Cell Cycle Regulation of Spindle Elongation. Developmental Cell, 2009, 17, 244-256.	3.1	121
29	Assembling the spindle midzone in the right place at the right time. Cell Cycle, 2008, 7, 283-286.	1.3	38
30	Cdc14-regulated midzone assembly controls anaphase B. Journal of Cell Biology, 2007, 177, 981-993.	2.3	143